

02/05

#2



OIPÉ

#2

RAW SEQUENCE LISTING

DATE: 01/29/2002

PATENT APPLICATION: US/10/038,241

TIME: 11:58:53

Input Set : A:\00-94.SEQ.txt

Output Set: N:\CRF3\01292002\J038241.raw

PS

3 <110> APPLICANT: Conklin, Darrell C.
 4 Gao, Zeren
 5 Lofton-Day, Catherine E.
 6 Whitmore, Theodore E.
 8 <120> TITLE OF INVENTION: SECRETED ALPHA-HELICAL PROTEIN ZLMDA24
 11 <130> FILE REFERENCE: 00-94
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/038,241
 C--> 13 <141> CURRENT FILING DATE: 2001-10-19
 13 <150> PRIOR APPLICATION NUMBER: US 60/242,023
 14 <151> PRIOR FILING DATE: 2000-10-20
 16 <160> NUMBER OF SEQ ID NOS: 25
 18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1041
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (205)...(966)
 29 <400> SEQUENCE: 1

30	ctgagaacac cagaggactg gcagttggga gcctgatgga ggacaagtag ggcctcgagg	60
31	acaggtgcgt gacagaagca caggaaaaaa aagaaaaatg aagaaataaa aacacgagtt	120
32	catcagtaaa gaggtaccct ggcagcataa atattatgat aagctaaaaag ctggaatcat	180
33	ctggaaaaat aaataagact cctc atg tcc ttt tcg gtc cat aac cag aag	231
34	Met Ser Phe Ser Val His Asn Gln Lys	
35	1 5	
37	ggc agc aaa agg cct ttg cca ctg gaa cct ctt ctt ttt ctc caa gtc	279
38	Gly Ser Lys Arg Pro Leu Pro Leu Glu Pro Leu Leu Phe Leu Gln Val	
39	10 15 20 25	
41	cca cgt agc aat tac ctg cac ttt caa gaa gag aaa caa cga cta cac	327
43	Pro Arg Ser Asn Tyr Leu His Phe Gln Glu Lys Gln Arg Leu His	
44	30 35 40	
46	cta aag aaa ttc ctt ctt gat agg atg ttt cta gtg gcc aag ata caa	375
47	Leu Lys Lys Phe Leu Leu Asp Arg Met Phe Leu Val Ala Lys Ile Gln	
48	45 50 55	
50	gca aat gta gaa aga aaa gat gtt gct gac tac tat gaa caa atg ttt	423
51	Ala Asn Val Glu Arg Lys Asp Val Ala Asp Tyr Tyr Glu Gln Met Phe	
52	60 65 70	
54	cag tca gtt ttg aaa cat cac cta gga gaa gca gtg aca gga ttg ctg	471
55	Gln Ser Val Leu Lys His His Leu Gly Glu Ala Val Thr Gly Leu Leu	
56	75 80 85	
58	ctc atc tat ccc act tcc att ctg cat atc ctc gag tcc tcc agc gac	519
59	Leu Ile Tyr Pro Thr Ser Ile Leu His Ile Leu Glu Ser Ser Ser Asp	

ENTERED

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```

60      90                      95                      100                      105
62 act ctc tac aaa gtt ctt tta gat tat att ggc cat gtc aaa gat gaa      567
63 Thr Leu Tyr Lys Val Leu Leu Asp Tyr Ile Gly His Val Lys Asp Glu
64                      110                      115                      120
66 aca gta ttt ttt att caa caa atg aaa att ata gtc att tct cat aac      615
67 Thr Val Phe Phe Ile Gln Gln Met Lys Ile Ile Val Ile Ser His Asn
68                      125                      130                      135
70 att cca atg agg ctt ttt atg caa tgg cat gtt tca gtg ata aaa gtt      663
71 Ile Pro Met Arg Leu Phe Met Gln Trp His Val Ser Val Ile Lys Val
72                      140                      145                      150
74 cca gtt atg tat ctc gac gat gtg aca cag tca cag tcc cta aag gag      711
75 Pro Val Met Tyr Leu Asp Asp Val Thr Gln Ser Gln Ser Leu Lys Glu
76                      155                      160                      165
78 gtc atc aca gat ttt ctc aca caa act cat aaa ctg tca ctc tac ctt      759
79 Val Ile Thr Asp Phe Leu Thr Gln Thr His Lys Leu Ser Leu Tyr Leu
80 170                      175                      180                      185
82 tgc cag act atg aaa gta ggc act aaa gga cca ggc gat aac tta cac      807
83 Cys Gln Thr Met Lys Val Gly Thr Lys Gly Pro Gly Asp Asn Leu His
84                      190                      195                      200
86 caa gtt gca cct gac cta ctc ctc cca gaa caa atc ata aag tac ttg      855
87 Gln Val Ala Pro Asp Leu Leu Leu Pro Glu Gln Ile Ile Lys Tyr Leu
88                      205                      210                      215
90 tgc aaa tcc gaa gaa ttc atg gac ccg gca aca ttt ata aac atg tat      903
91 Cys Lys Ser Glu Glu Phe Met Asp Pro Ala Thr Phe Ile Asn Met Tyr
92                      220                      225                      230
94 aat aga ccc ata cac atc act ctg gat tct gag gtg gta tgg cct gct      951
95 Asn Arg Pro Ile His Ile Thr Leu Asp Ser Glu Val Val Trp Pro Ala
96                      235                      240                      245
98 cct tca cgt ttc tag gattgagagg gataatgtgc ccatgtctct taaggagttt      1006
99 Pro Ser Arg Phe *
100 250
102 gtgctactta aataaaaaaaaa acattttttaa agtta      1041
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 253
106 <212> TYPE: PRT
107 <213> ORGANISM: Human
109 <400> SEQUENCE: 2
110 Met Ser Phe Ser Val His Asn Gln Lys Gly Ser Lys Arg Pro Leu Pro
111 1 5 10 15
112 Leu Glu Pro Leu Leu Phe Leu Gln Val Pro Arg Ser Asn Tyr Leu His
113 20 25 30
114 Phe Gln Glu Glu Lys Gln Arg Leu His Leu Lys Lys Phe Leu Leu Asp
115 35 40 45
116 Arg Met Phe Leu Val Ala Lys Ile Gln Ala Asn Val Glu Arg Lys Asp
117 50 55 60
118 Val Ala Asp Tyr Tyr Glu Gln Met Phe Gln Ser Val Leu Lys His His
119 65 70 75 80
120 Leu Gly Glu Ala Val Thr Gly Leu Leu Leu Ile Tyr Pro Thr Ser Ile
121 85 90 95

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Input Set : A:\00-94.SEQ.txt

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```

122 Leu His Ile Leu Glu Ser Ser Ser Asp Thr Leu Tyr Lys Val Leu Leu
123           100           105           110
124 Asp Tyr Ile Gly His Val Lys Asp Glu Thr Val Phe Phe Ile Gln Gln
125           115           120           125
126 Met Lys Ile Ile Val Ile Ser His Asn Ile Pro Met Arg Leu Phe Met
127           130           135           140
129 Gln Trp His Val Ser Val Ile Lys Val Pro Val Met Tyr Leu Asp Asp
130           145           150           155           160
131 Val Thr Gln Ser Gln Ser Leu Lys Glu Val Ile Thr Asp Phe Leu Thr
132           165           170           175
133 Gln Thr His Lys Leu Ser Leu Tyr Leu Cys Gln Thr Met Lys Val Gly
134           180           185           190
135 Thr Lys Gly Pro Gly Asp Asn Leu His Gln Val Ala Pro Asp Leu Leu
136           195           200           205
137 Leu Pro Glu Gln Ile Ile Lys Tyr Leu Cys Lys Ser Glu Glu Phe Met
138           210           215           220
139 Asp Pro Ala Thr Phe Ile Asn Met Tyr Asn Arg Pro Ile His Ile Thr
140           225           230           235           240
141 Leu Asp Ser Glu Val Val Trp Pro Ala Pro Ser Arg Phe
142           245           250
144 <210> SEQ ID NO: 3
145 <211> LENGTH: 1056
146 <212> TYPE: DNA
147 <213> ORGANISM: Mus musculus
149 <220> FEATURE:
150 <221> NAME/KEY: CDS
151 <222> LOCATION: (106)...(867)
153 <400> SEQUENCE: 3
154 gcagagggtca agccaagagg acctcagacc tcaaagacag aaataaaaaat aagaattcac      60
155 taccattgag acttgtaatc atctaaaaaaa gaaataagat tcatc atg tct ttc atg      117
156                               Met Ser Phe Met
157                               1
159 gtc cat aat cgg aag ggc agc aaa aag caa ttt caa gtg gat cct ctt      165
160 Val His Asn Arg Lys Gly Ser Lys Lys Gln Phe Gln Val Asp Pro Leu
161   5           10           15           20
163 ctt ctg ccc aag gtt cct cgt acc aat tac ctg cac ctt cag gaa gag      213
164 Leu Leu Pro Lys Val Pro Arg Thr Asn Tyr Leu His Leu Gln Glu Glu
165           25           30           35
167 aag cac aga cta cag cta aag aaa ttc ctc ctt cac agg atg ttt cta      261
168 Lys His Arg Leu Gln Leu Lys Lys Phe Leu Leu His Arg Met Phe Leu
169           40           45           50
171 gtg ggc tac ata caa ggc aac acg gag aaa aag gac atc tct gag tac      309
172 Val Gly Tyr Ile Gln Gly Asn Thr Glu Lys Lys Asp Ile Ser Glu Tyr
173           55           60           65
175 tat gag caa ctg ttt cag tca att ctg aaa cat cat tta ggc gaa tca      357
176 Tyr Glu Gln Leu Phe Gln Ser Ile Leu Lys His His Leu Gly Glu Ser
177           70           75           80
179 gtg aca ggt ctc atg ctc gta tac cca agt act ttt ctg cac att ctt      405
180 Val Thr Gly Leu Met Leu Val Tyr Pro Ser Thr Phe Leu His Ile Leu

```

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```

181      85                      90                      95                      100
183 gag agt tcc aat ggc aca ctc ttc cgg att ctt cta gat tat gtt gcc      453
184 Glu Ser Ser Asn Gly Thr Leu Phe Arg Ile Leu Leu Asp Tyr Val Ala
185                      105                      110                      115
187 cat gaa aag agt gaa aca gaa ttt atg ctc caa aac atg aaa atc gtt      501
188 His Glu Lys Ser Glu Thr Glu Phe Met Leu Gln Asn Met Lys Ile Val
189                      120                      125                      130
191 gtt gct tct cac aac atc ccc acg agg ctg ttc atg cag tgg cat atc      549
192 Val Ala Ser His Asn Ile Pro Thr Arg Leu Phe Met Gln Trp His Ile
193                      135                      140                      145
195 tct gca atc aaa gtc ccc gtt ttg tac cta gat gac gaa tca cag tct      597
196 Ser Ala Ile Lys Val Pro Val Leu Tyr Leu Asp Asp Glu Ser Gln Ser
197                      150                      155                      160
199 ccg tct ata gag gaa gtc acc aca gaa ttc ctc acc atg act cac aaa      645
200 Pro Ser Ile Glu Glu Val Thr Thr Glu Phe Leu Thr Met Thr His Lys
201 165                      170                      175                      180
203 ctg gca ctc caa ctt tac aag aca gtg aaa ttg ggc gcg aaa ggt cca      693
204 Leu Ala Leu Gln Leu Tyr Lys Thr Val Lys Leu Gly Ala Lys Gly Pro
205                      185                      190                      195
207 ggt gac aac tta cac caa ctt gcc cct gaa ctc att ctc cca gaa caa      741
208 Gly Asp Asn Leu His Gln Leu Ala Pro Glu Leu Ile Leu Pro Glu Gln
209                      200                      205                      210
211 att atc aag tat tta tgc aaa gct gaa gaa ttc atg gac cca gcg tct      789
212 Ile Ile Lys Tyr Leu Cys Lys Ala Glu Glu Phe Met Asp Pro Ala Ser
213                      215                      220                      225
215 ttc ttg agc atg tat aac aga ccc ata cac gtt acc ctg gat tcc gat      837
216 Phe Leu Ser Met Tyr Asn Arg Pro Ile His Val Thr Leu Asp Ser Asp
217                      230                      235                      240
219 att gtg tgg cca gct cct tcc cgt ttc tag aatggggaga gttgatttgg      887
220 Ile Val Trp Pro Ala Pro Ser Arg Phe *
221 245                      250
223 agaggatgtc tacaacattc agaagcattg aagatggcac cagagcagga gggtgaaaga      947
224 acgcatgttc agccaggcat agaacaggag ccaggaaggg gacaacacca taaattcctg      1007
225 aatttctttg tgttttaggc actaaacata ataaatttct taagactga      1056
227 <210> SEQ ID NO: 4
228 <211> LENGTH: 253
229 <212> TYPE: PRT
230 <213> ORGANISM: Mus musculus
232 <400> SEQUENCE: 4
233 Met Ser Phe Met Val His Asn Arg Lys Gly Ser Lys Lys Gln Phe Gln
234 1                      5                      10                      15
235 Val Asp Pro Leu Leu Pro Lys Val Pro Arg Thr Asn Tyr Leu His
236                      20                      25                      30
237 Leu Gln Glu Glu Lys His Arg Leu Gln Leu Lys Lys Phe Leu Leu His
238                      35                      40                      45
239 Arg Met Phe Leu Val Gly Tyr Ile Gln Gly Asn Thr Glu Lys Lys Asp
240 50                      55                      60
241 Ile Ser Glu Tyr Tyr Glu Gln Leu Phe Gln Ser Ile Leu Lys His His
242 65                      70                      75                      80

```

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```

243  Leu Gly Glu Ser Val Thr Gly Leu Met Leu Val Tyr Pro Ser Thr Phe
244                      85                      90                      95
245  Leu His Ile Leu Glu Ser Ser Asn Gly Thr Leu Phe Arg Ile Leu Leu
246                      100                     105                     110
247  Asp Tyr Val Ala His Glu Lys Ser Glu Thr Glu Phe Met Leu Gln Asn
248                      115                     120                     125
249  Met Lys Ile Val Val Ala Ser His Asn Ile Pro Thr Arg Leu Phe Met
250                      130                     135                     140
251  Gln Trp His Ile Ser Ala Ile Lys Val Pro Val Leu Tyr Leu Asp Asp
252  145                      150                      155                      160
253  Glu Ser Gln Ser Pro Ser Ile Glu Glu Val Thr Thr Glu Phe Leu Thr
254                      165                      170                      175
255  Met Thr His Lys Leu Ala Leu Gln Leu Tyr Lys Thr Val Lys Leu Gly
256                      180                      185                      190
258  Ala Lys Gly Pro Gly Asp Asn Leu His Gln Leu Ala Pro Glu Leu Ile
259                      195                      200                      205
260  Leu Pro Glu Gln Ile Ile Lys Tyr Leu Cys Lys Ala Glu Glu Phe Met
261                      210                      215                      220
262  Asp Pro Ala Ser Phe Leu Ser Met Tyr Asn Arg Pro Ile His Val Thr
263  225                      230                      235                      240
264  Leu Asp Ser Asp Ile Val Trp Pro Ala Pro Ser Arg Phe
265                      245                      250
267 <210> SEQ ID NO: 5
268 <211> LENGTH: 759
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Degenerate polynucleotide sequence of human zlmada24
274      shown in SEQ ID NO:2
276 <221> NAME/KEY: misc_feature
277 <222> LOCATION: (1)...(759)
278 <223> OTHER INFORMATION: n = A,T,C or G
280 <400> SEQUENCE: 5
W--> 281  atgwsnttyw sngtncayaa ycaraarggn wsnaarmgnc cnytnccnyt ngarccnytn      60
W--> 282  ytnnttytnc argtnccnmg nwsnaaytay ytncaytttc argargaraa rcarmgnytn      120
W--> 283  cayytnaara arttyytnyt ngaymgnatg ttyytngtng cnaarathca rgcnaaygtn      180
W--> 284  garmgnaarg aygtngcnga ytaytaygar caratgttyc arwsngtnyt naarcaycay      240
W--> 285  ytnggngarg cngtnacngg nytnytnytn athtayccna cnwsnathyt ncayathytn      300
W--> 286  garwsnwnw sngayacnyt ntayaargtn ytnytnngayt ayathggncay ygtnaargay      360
W--> 287  garacngtnt tyttyathca rcaratgaar athathgtna thwsncayaa yathccnatg      420
W--> 288  mgnytnttya tgcartggca ygtnwsngtn athaargtnw sngtnatgta yytngaygay      480
W--> 289  gtnacncarw sncarwsnyt naargargtn athacngayt tyytnacnca racncayaar      540
W--> 290  ytnwsnytn ayytntgyca racnatgaar gtnggnacna arggncncng ngayaayytn      600
W--> 291  caycargtng cncngayyt nytnytnccn garcaratha thaartayyt ntgyaarwsn      660
W--> 292  gargarttya tggayccngc nacttyyath aayatgtaya aymgncnat hcayathacn      720
W--> 293  ytngaywsng argtngtntg gccngcncn wsnmgntty      759
295 <210> SEQ ID NO: 6
296 <211> LENGTH: 759
297 <212> TYPE: DNA

```

→ Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/038,241

DATE: 01/29/2002

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Input Set : A:\00-94.SEQ.txt

Output Set: N:\CRF3\01292002\J038241.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6